



Form PTO 1449		
ATTY DOCKET NO. 64-98A	SERIAL NO. 09/839,884	FILING DATE: April 20, 2001
APPLICANT: Aebersold et al.		GROUP: 1632

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U.S. PATENT DOCUMENTS

Exmr Initial		Document Number	Date	Name	Class	Subclass	Filing Date if Appropriate
86	1	6,017,693	01/25/00	Yates, III et al.	435	5	
86	2	5,952,653	09/14/99	Covey et al.	250	288	
86	3	5,686,310	11/11/97	Haystead et al	436	86	
86	4	5,650,270	07/22/97	Giese et al.	435	6	
86	5	5,538,897	07/23/96	Yates, III et al.	436	89	
86	6	5,240,859	08/31/93	Aebersold	436	89	

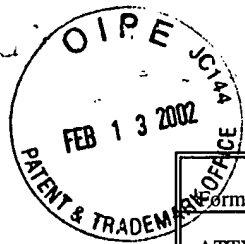
FOREIGN PATENT DOCUMENTS

		Document Number	Date	Country	Class	Subclass	Translation Yes/No
86	7	WO98/26095	06/18/98	PCT	C12Q	1/68	✓
86	8	WO 01/96869 A1	20/12/01	WO	G01N	33/53	✓

OTHER PRIOR ART (including Author, Title, Date, Pertinent Pages, etc.)

86	9		Aebersold, R. et al. (1991) "Determination of the site of tyrosine phosphorylation at the low picomole level by automated solid-phase sequence analysis" <i>Anal. Biochem.</i> 199 :51-60
86	10		Bennetzen, J.L. and Hall, B.D. , "Codon Selection in Yeast," (March 1982) <i>J. Biol. Chem.</i> 257 (6):3026-3031
86	11		Boucherie, H. et al. (1996) "Two-dimensional gel protein database of <i>Saccharomyces cerevisiae</i> " <i>Electrophoresis</i> 17 :1683-1699
86	12		Bruce, J. E. et al. (January 2000) "Obtaining More Accurate FTICR Mass Measurements Without Internal Standards using Multiply Charged Ions" <i>J. Am. Soc. Mass Spec.</i> 11 (5):416-421
86	13		Bruce, J.E. et al. (July 1999) "High-Mass-Measurement Accuracy and 100% Sequence Coverage of Enzymatically Digested Bovine Serum Albumin from an ESI-FTICR Mass Spectrum" <i>Anal. Chem.</i> 71 (14):2595-2599

EXAMINER <i>Grilene R. Gehl</i>	DATE CONSIDERED <i>5/17/02</i>
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<i>ff</i>	14	Davis, T. et al. (March 1998) "Rapid Protein Identification Using a Microscale Electrospray LC/MS System on an Ion Trap Mass Spectrometer," <i>J. Am. Soc. Mass. Spec.</i> 9 :194-201
<i>ff</i>	15	Fenyo, D. et al. (May 1998) "Protein identification using mass spectrometric information," <i>Electrophoresis</i> 19 :998-1005
<i>ff</i>	16	Fraser, C.M. et al. (Dec 1997) "Genomic sequence of a Lyme disease spirochaete, <i>Borrelia burgdorferi</i> ," <i>Nature</i> 390 :580-586
<i>ff</i>	17	Futcher, B. et al. (November 1999) "A Sampling of the Yeast Proteome" <i>Mol. Cell. Bio.</i> 19 (11):7357-7368
<i>ff</i>	18	Gingras, A.C. et al. (June 1999) "Regulation of 4E-BP1 phosphorylation: a novel two-step mechanism" <i>Genes Dev.</i> 13 :1422-1437
<i>ff</i>	19	Goffeau et al. (Oct 1996) "Life with 6000 Genes," <i>Science</i> 274 :546-549
<i>ff</i>	20	Goodlett et al. (1993), "Reduced Elution Speed Detection for Capillary Electrophoresis/Mass Spectrometry" <i>J. Microcolumn Separations</i> 5 :57-62
<i>ff</i>	21	Goodlett, D.R. et al. (March 2000) "Protein identification with a single accurate mass of a cysteine-containing peptide and constrained database searching" <i>Anal. Chem.</i> 72 (6):1112-1118
<i>ff</i>	22	Goodlett, D.R. et al. (March 2000) "Quantitative in Vitro kinase reaction as a guide for phosphoprotein analysis by mass spectrometry" <i>Rapid Commun Mass Spectrom.</i> 14 (5):344-348
<i>ff</i>	23	Graves, J.D. & Krebs, ED. (May 1999) "Protein phosphorylation and signal transduction" <i>Pharmacol. Ther.</i> 82 :(2-3)111-121
<i>ff</i>	24	Gygi, S.P. and Aebersold, R. (October 2000) "Mass spectrometry and proteomics" <i>Curr. Opin. Chem. Biol.</i> 4 (5):489-94
<i>ff</i>	25	Gygi, S.P. et al. (August 2000) "Measuring gene expression by quantitative proteome analysis" <i>Curr. Opin. Biotechnol.</i> 11 (4):396-401
<i>ff</i>	26	Haynes, P.A. et al. (1998) "Proteome Analysis: Biological Assay or Data Archive?" <i>Electrophoresis Vol.</i> 19 :1862-1871
<i>ff</i>	27	Henzel, W.J. et al. (June 1993) "Identifying proteins from two-dimensional gels by molecular mass searching of peptide fragments in protein sequence databases," <i>Proc. Natl. Acad. Sci. USA</i> 90 :5011-5015

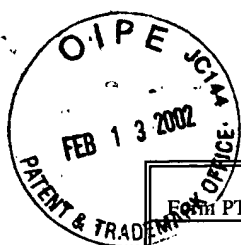
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Priscilla B. Z...

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88	28	Horn, D. M. et al. (1998) "A Computer Program for Automated Analysis of High Resolution Mass Spectra," <i>Proceedings of the 46th ASMS Conf. on Mass Spectrometry and Allied Topics</i> , Orlando, FL May 31 - June 4, 1998, p.118
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88	34	Link, J. et al. (July 1999) "Direct analysis of protein complexes using mass spectrometry," <i>Nat. Biotech.</i> 17:676-682
88	35	Lundell, N. and Schreitmuller, T. (January 1999) "Sample Preparation for Peptide Mapping - A Pharmaceutical Quality-Control Perspective," <i>Anal. Biochem.</i> 266:31-47
88	36	Marshall et al. (May 1998) "Fourier Transform Ion Cyclotron Resonance Mass Spectrometry: A Primer," <i>Mass. Spectrom. Rev.</i> 17:1-35
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88	39	Neubauer, G. et al. (Sept 1998) "Mass spectrometry and EST-database searching allows characterization of the multi-protein spliceosome complex," <i>Nature Genetics</i> 20:46-50
88	40	Ogryzko, Vasily V. et al. (July 10, 1998), "Histone-like TAFs within the PCAF Histone Acetylase Complex" <i>Cell</i> 94:35-44.
88	41	Papayannopoulos, I.A. (1995) "The interpretation of collision-induced dissociation tandem mass spectra of peptides" <i>Mass Spectrometry Rev.</i> 14:49-73

EXAMINER	<i>Priscilla R. Gould</i>	DATE CONSIDERED	<i>5/17/02</i>
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42	Patterson, S.D. and Aebersold, R. (1995) "Mass spectrometric approaches for identification of gel-separated proteins," <i>Electro.</i> 16 :1791-1814
43	Qin, J. et al. (January 1998) "De Novo Peptide Sequencing in an Ion Trap Mass Spectrometer with ¹⁸ O Labeling" <i>Rapid Communications in Mass Spectrometry</i> 12 :209-216
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EXAMINER <i>Erilene R. Brubaker</i>	DATE CONSIDERED <i>5/17/02</i>
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